

Access DB# 164534

CRFE

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 8/31/05  
Art Unit: 1636 Phone Number 302 272-0767 Serial Number: 10/643627  
Mail Box and Bldg/Room Location: Room 2A79 Results Format Preferred (circle): PAPER DISK E-MAIL  
Mailbox: 2C70

If more than one search is submitted, please prioritize searches in order of need.

mej

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Here search for fragments of SEQ ID NO: 4  
or SEQ ID NO: 6 at least 10 consecutive amino  
acids in length or at least 40 consecutive  
amino acids in length.

4 aa 398

6 aa 398

Thanks

mej

9/16/05  
FTH

## STAFF USE ONLY

Searcher: Beverly 2528

Type of Search

Vendors and cost where applicable

NA Sequence (#)

STN

OFFICIAL USE ONLY

165100

ACCESS DB #

PLEASE PRINT CLEARLY

10

Scientific and Technical Information Center

# SEARCH REQUEST FORM

CRFB

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 9/8/05  
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/643627  
Location (Bldg/Room#): Room 2A79 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

## Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for fragments of SEQ ID NO: 63  
at least 10 consecutive amino acids in length or  
at least 20 consecutive amino acids in length or at  
least 40 consecutive amino acids in length.

63-397 A1A

Complete  
9/15/05  
J.H.

T. Banks

RECEIVED  
SEP - 8 2005  
TECH/CHEM. DIVISION  
(STIC)

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:01:04 ; Search time 170 Seconds

(without alignments)  
903.199 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397  
Sequence: 1 MRSPSAAMLGAAILLAASL.....KHSRKSSTSSSTTVKTSY 397

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 40

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: A\_Geneseq\_1Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	296	74.6	397	2	AAR6923 Human C14
2	296	74.6	397	2	AAW01955 Human C14
3	114	28.7	394	2	AAW51408 Human pro
4	114	28.7	397	3	AAW55641 Human PAR
5	114	28.7	397	5	AAE26678 Human coa
6	114	28.7	397	6	ABG73508 Human par
7	114	28.7	397	7	ADBE2812 Human pro
8	114	28.7	397	8	ADL61221 Human coa
9	114	28.7	397	8	AD029311 Human GPC
10	114	28.7	397	8	AD574020 Human G-P
11	114	28.7	398	2	AAR6921 Human C14
12	114	28.7	398	2	AAW01953 Human C14
13	91	22.9	320	8	AD128655 Human mod
14	91	22.9	341	8	AD128654 Human mod
15	91	22.9	355	8	AD128653 Human mod
16	91	22.9	397	6	ABP81907 Human pro
17	91	22.9	397	7	ADK52594 Hematolog
18	91	22.9	397	7	ADN39997 Cancer/an
19	91	22.9	397	8	ADR46675 Cancer-as
20	57	14.4	389	8	ADO28601 Human PAR

## ALIGNMENTS

### RESULT 1

AAR6923 standard; protein: 397 AA.

AC AAR6923;

DT 25-MAR-2003 (revised)

DT 22-AUG-1995 (first entry)

DE Human C140 receptor encoded by cDNA.

KW G-protein-coupled receptor; G-protein; C140 receptor.

OS Homo sapiens.

PN MO9503318-A1.

PD 02-FEB-1995.

PF 26-JUL-1994; 94WO-US008536.

PR 26-JUL-1993; 93US-00097938.

PA (CORT-) COR THERAPEUTICS.

PI Scarborough RM, Sundelin J;

DR WPI; 1995-075182/10.

DR N-PSDB; AA084560.

PT New DNA encoding recombinant C140 receptor - and novel agonists and antagonists and specific antibodies with therapeutic and diagnostic applications.

PS Example; Fig 11; 57pp; English.

XX A human intestinal tumor cDNA library was subjected to PCR using primers

CC designed from the genomic clone (see AA084558) and the amplified fragment

CC was cloned in pSDS and sequenced. There are four AA differences between

CC the cDNA encoded sequence and that encoded by the genomic DNA. The

CC cDNA sequence and deduced AA sequence are given in AA084560 &

CC AAR6923. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 397 AA;

Query Match 74.6%; Score 296; DB 2; Length 397;

Best Local Similarity 99.7%; Pred. No. 2.9e-276;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MRSPSAAMLGAAILLAASLCSGTTIOGTRSSKGRSLIGKVDGSHVTKGVETFS	60
DB	1	MRSPSAAMLGAAILLAASLCSGTTIOGTRSSKGRSLIGKVDGSHVTKGVETFS	60
QY	61	VDEPFAVLAGLTVPLPIVTVIVAVGLPENGMAWFLPRTKKGPAVIYMANLALA	120
DB	61	VDEPFAVLAGLTVPLPIVTVIVAVGLPENGMAWFLPRTKKGPAVIYMANLALA	120
QY	121	DLSAVIWPFLKTAHYHGNMNYGEALCNVLGFFYGNMNYCSILEFTCLSVORVYVNP	180
DB	121	DLSAVIWPFLKTAHYHGNMNYGEALCNVLGFFYGNMNYCSILEFTCLSVORVYVNP	180
QY	181	MGRSRKKAIAIGISLAWLTLVLPYVVKQTFIPALNITTCDDVLPQOLVGDWF	240
DB	181	MGRSRKKAIAIGISLAWLTLVLPYVVKQTFIPALNITTCDDVLPQOLVGDWF	240
QY	241	NYFLSLAIGVFLPFAVFLTASAVYLMIRMSAMDENSKKRRAIKLIVTVLGWYICF	300
DB	241	NYFLSLAIGVFLPFAVFLTASAVYLMIRMSAMDENSKKRRAIKLIVTVLGWYICF	300
QY	301	TPSNLLLVVHYFLIKSGQSHVYALYIVALCLSTLNSCIDPFYVYVSHDFPDHAKNAL	360
DB	301	TPSNLLLVVHYFLIKSGQSHVYALYIVALCLSTLNSCIDPFYVYVSHDFPDHAKNAL	360

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## OM protein - protein search, using sw model

Run on: September 15, 2005, 09:14:51 ; Search time 41 Seconds

(without alignments)  
931.660 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397

Sequence: 1 MRSPSAAMLGAILLAASL.....KHSRKSSSYSSSTVTYKTSY 397

Scoring table: OLIGO

Searched: 283416 seqs, 9621673 residues

Word size: 10

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: PIR 79:\*

1: pir1:\*\n2: pir2:\*\n3: pir3:\*\n4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	28.7	397	2 S66518	proteinase-activat
2	34	8.6	399	2 148705	proteinase activat
3	10	2.5	425	2 A37912	thrombin receptor
4	10	2.5	427	2 S17148	alpha-thrombin rec
5	10	2.5	432	2 A43448	thrombin receptor

## ALIGNMENTS

RESULT 1  
S66518  
proteinase-activated receptor 2 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S66518; S64709; G02131  
R/Nystedt, S.; Emlison, K.; Larsen, A.K.; Strombeck, B.; Sundelin, J.  
Eur. J. Biochem. 232, 84-89, 1995  
A/Title: Molecular cloning and functional expression of the gene encoding the human prot  
A/Reference number: S66518; MUID:96048032; PMID:7556175  
A/Accession: S66518  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-397 <NTS>  
A/Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:G106084; PIDN:CAA90290.1; PID:G100  
R/Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn  
Biochem. J. 314, 1009-1016, 1996  
A/Title: Molecular cloning, expression and potential functions of the human proteinase-  
A/Reference number: S64709; MUID:96177879; PMID:8615752

A/Accession: S64709  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-137, 'A', 139-397 <BOE>  
A/Cross-references: EMBL:U34038; NID:G1041728; PIDN:AA847871.1; PID:G1041729  
A/Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residue  
R/Kahn, M.L.; Coughlin, S.R.  
Submitted to the EMBL Data Library, September 1995  
A/Reference number: H00822  
A/Accession: G02131  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 25-397 <KAH>  
A/Cross-references: EMBL:U36753; NID:G1208539; PIDN:AAA90957.1; PID:G1208540  
C/Genetics:  
A/Map position: 5q13  
A/Intons: 28/1  
C/Superfamily: ATP receptor P2u  
F,1-36/Domain: activation peptide #status predicted <APT>  
F,1-25/Domain: signal sequence #status predicted <SIG>  
F,37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 28.7%; Score 114; DB 2; Length 397;  
Best Local Similarity 100.0%; Pred. No. 4.1e-105;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 VGLPSNGMALWVLEFRTKKGPVIVMANLADLLSVIFPLKIAVHIGNWYGEAL 147  
DB 88 VGLPSNGMALWVLEFRTKKGPVIVMANLADLLSVIFPLKIAVHIGNWYGEAL 147

QY 148 CNVLIQFFYGNMYCSILFMTCISVQRYVIVNWMGSRKKANAIIGSLAIWLL 201  
DB 148 CNVLIQFFYGNMYCSILFMTCISVQRYVIVNWMGSRKKANAIIGSLAIWLL 201

## RESULT 2

148705  
proteinase activated receptor 2 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: 148705  
R/Nystedt, S.; Larsen, A.K.; Aberg, H.; Sundelin, J.  
J. Biol. Chem. 270, 5950-5955, 1995  
A/Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and  
A/Reference number: 148705; MUID:95197620; PMID:7890726  
A/Accession: 148705  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-399 <RBS>  
A/Cross-references: UNIPROT:P55086; EMBL:Z48043; NID:G663020; PIDN:CAA88097.1; PID:G663  
C/Superfamily: ATP receptor P2u

Query Match 8.6%; Score 34; DB 2; Length 399;  
Best Local Similarity 100.0%; Pred. No. 1.8e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 VLIQFFYGNMYCSILFMTCISVQRYVIVNPMGH 183  
DB 152 VLIQFFYGNMYCSILFMTCISVQRYVIVNPMGH 185

## RESULT 3

A37912  
thrombin receptor precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text\_change 09-Jul-2004  
C/Accession: A37912  
R/Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.  
Cell 64, 1057-1068, 1991  
A/Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolyti  
A/Reference number: A37912; MUID:91168254; PMID:1672265  
A/Accession: A37912  
A/Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:14:06; Search time 169 Seconds

(without alignments)  
1202.932 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397  
Sequence: 1 MRSPSAWMLGAILLNLASL.....KHSRKSSSYSSSTTVKTSY 397

Scoring table: OLGPO  
Gapop 60.0, Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size: 10

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database: Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	28.7	397	1	PAR2_HUMAN
2	37	9.3	397	1	PAR2_RAT
3	34	8.6	399	1	PAR2_MOUSE
4	34	8.6	399	1	PAR2_MOUSE
5	10	2.5	90	2	QBR311
6	10	2.5	374	1	PAR3_HUMAN
7	10	2.5	376	2	Q723W3
8	10	2.5	425	1	PAR1_HUMAN
9	10	2.5	425	1	PAR1_PAPHA
10	10	2.5	428	1	PAR1_CRILLO
11	10	2.5	430	1	PAR1_MOUSE
12	10	2.5	432	1	PAR1_MOUSE
					P26824 ratmus norv

## ALIGNMENTS

RESULT 1  
PAR2\_HUMAN  
ID PAR2\_HUMAN STANDARD; PRT; 397 AA.  
AC P55086; Q13317; Q13346;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Proteinase activated receptor 2 precursor (PAR-2) (thrombin receptor-like 1) (Coagulation factor II receptor-like 1).  
GN Name=PAR2; Synonyms=GPRI1, PAR2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_Taxid=9606;

RP [1]  
RX SEQUENCE FROM N.A.  
RA MEDLINE=96048032; PubMed=7556175;  
RT Nystedt S., Emilsson K., Larsson A.-K., Strombeck B., Sundelin J.;  
RL "Molecular cloning and functional expression of the gene encoding the human proteinase-activated receptor 2.";  
RM Eur. J. Biochem. 232:84-89(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Kidney;  
RA MEDLINE=96177879; PubMed=8615752;  
RT Boehm S.K., Kong W., Broemme D., Smeekens S.P., Anderson D.C.,  
RL Connolly A.J., Kahn M.L., Nelken N.A., Coughlin S.R., Payan D.G.,  
RN Bunnett N.W.;  
RP "Molecular cloning, expression and potential functions of the human proteinase-activated receptor-2.";  
RL Biochem. J. 314:1009-1016(1996).  
RN [3]  
RP SEQUENCE OF 29-397 FROM N.A.  
RX MEDLINE=96379236; PubMed=8784787;  
RA Kahn M.L., Ishii K., Kuo W.L., Piper M., Connolly A.J., Shi Y.P.,  
RL Mu R., Lin C.C., Coughlin S.R.;  
RP "Conserved structure and adjacent location of the thrombin receptor and protease-activated receptor 2 genes define a protease-activated receptor gene cluster.";  
RL Mol. Med. 2:349-357(1996).  
RN [4]  
RP SEQUENCE FROM N.A. AND VARIANTS PHE-21; GLN-270 AND ALA-291.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RL Nickerson D.A.;  
RT "SeattleSNPs: NHLBI H66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Ovary, and Pancreas;  
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hale F.,  
RA Diatzenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,  
RA Sabetlen M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;  
RP "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP FUNCTION: Receptor for trypsin and trypsin-like enzymes coupled to G proteins that stimulate phosphoinositide hydrolysis. May have a role in the regulation of vascular tone.  
RN [7]  
RP SUBCELLULAR LOCATION: Integral membrane protein.  
RN [8]  
RP TISSUE SPECIFICITY: Widely expressed in tissues with especially high levels in pancreas, liver, kidney, small intestine, and colon. Moderate expression is detected in many organs, but none in brain or skeletal muscle.  
RN [9]  
RP PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.  
RN [10]  
RP SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
RN [11]  
RP This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

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OM protein - protein search, using sw model

Run on: September 15, 2005, 09:11:11 ; Search time 167 Seconds  
(without alignments)  
919.424 Million cell updates/sec

Title: US-10-643-627-63

Perfect score: 397  
Sequence: 1 MRSPSAWILGNAILLAAL.....KHSRKSSEYSSSTVTXTSY 397

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 10

Total number of hits satisfying chosen parameters: 87

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	296	74.6	397	2	AAW01955 Human C14
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4	114	28.7	397	3	AAW35641 Human PAR
5	114	28.7	397	5	AAE26678 Human coa
6	114	28.7	397	7	ABG73508 Human par
7	114	28.7	397	7	ADBE62812 Human pro
8	114	28.7	397	8	AD6161221 Human coa
9	114	28.7	397	8	AD029311 Human GPC
10	114	28.7	397	8	AD674020 Human G-P
11	114	28.7	398	2	AAR66921 Human C14
12	114	28.7	398	2	AAW01953 Human C14
13	114	28.7	320	8	AD128655 Human mod
14	91	22.9	341	8	AD128654 Human mod
15	91	22.9	355	8	AD128653 Human mod
16	91	22.9	397	6	ABP81907 Human pro
17	91	22.9	397	7	ADK52594 HematoLog
18	91	22.9	397	7	ADN39997 Cancer/an
19	91	22.9	397	8	ADR46675 Cancer-as
20	57	14.4	389	8	AD028601 Human PAR
21	39	9.8	54	8	AD128666 Human pro
22	37	9.3	397	7	AD662810 Rat Prote
23	34	8.6	395	2	AAR66920 Murine C1
24	34	8.6	395	2	AAW01952 Murine C1
25	34	8.6	399	2	AAR66922 Murine C1

26	34	8.6	399	2	AAW01954	AAW01954 Murine C1
27	34	8.6	399	7	ABR63562	ABR63562 Delayed h
28	34	8.6	399	8	AD029312	AD029312 Mouse GPC
29	33	8.3	58	5	ABU67239	ABU67239 G-protein
30	33	8.3	58	6	ABP54020	ABP54020 Human pro
31	33	8.3	58	8	AD028760	AD028760 Human pro
32	33	8.3	58	8	AD005264	AD005264 Proteins
33	25	6.3	25	3	AAV45037	AAV45037 Human pro
34	21	5.3	21	5	AAU10420	AAU10420 PAR2 pepd
35	20	5.0	20	6	ABP82705	ABP82705 G protein
36	20	5.0	21	5	AAU10421	AAU10421 PAR2 pepd
37	18	4.5	18	6	ABP82706	ABP82706 G protein
38	18	4.5	18	6	ABP82707	ABP82707 G protein
39	15	3.8	68	5	ADK35286	ADK35286 Novel hum
40	14	3.5	16	6	ABP82708	ABP82708 G protein
41	14	3.5	20	3	ABW35651	ABW35651 Human PAR
42	12	3.0	12	2	AAW76406	AAW76406 Human PAR
43	11	2.8	20	3	ABW35652	ABW35652 Mouse PAR
44	10	2.5	13	2	AAR66890	AAR66890 Agonist p
45	10	2.5	13	2	AAW01923	AAW01923 C140 rece
46	10	2.5	15	5	ABG35288	ABG35288 Human PAR
47	10	2.5	15	5	ABG35286	ABG35286 Human PAR
48	10	2.5	15	5	ABG35287	ABG35287 Human PAR
49	10	2.5	15	5	ABG35289	ABG35289 Human PAR
50	10	2.5	15	5	ABG35285	ABG35285 Human PAR
51	10	2.5	26	2	AAR27238	AAR27238 Thrombin
52	10	2.5	319	4	ABW82760	ABW82760 Rat G-pro
53	10	2.5	319	4	AD029401	AD029401 Mouse GPC
54	10	2.5	371	5	ABG35299	ABG35299 Human PAR
55	10	2.5	374	2	AAW51406	AAW51406 Human pro
56	10	2.5	374	6	ABG73509	ABG73509 Human par
57	10	2.5	374	6	ABP81908	ABP81908 Human pro
58	10	2.5	374	7	ADB67661	ADB67661 Human PAR
59	10	2.5	374	8	AD029313	AD029313 Human GPC
60	10	2.5	374	8	ADQ97469	ADQ97469 Human can
61	10	2.5	374	8	ADQ39889	ADQ39889 Human myo
62	10	2.5	374	8	ADG32990	ADG32990 Proteins
63	10	2.5	402	5	ABG35298	ABG35298 Human PAR
64	10	2.5	425	2	AAR27240	AAR27240 Human thr
65	10	2.5	425	2	ABR60698	ABR60698 Fragment
66	10	2.5	425	2	AAW51407	AAW51407 Human pro
67	10	2.5	425	2	AAV49570	AAV49570 Human thr
68	10	2.5	425	5	ABE17032	ABE17032 Human thr
69	10	2.5	425	5	ABG35300	ABG35300 Human PAR
70	10	2.5	425	5	ABG80697	ABG80697 Human thr
71	10	2.5	425	6	ABG73511	ABG73511 Human thr
72	10	2.5	425	6	ABR47449	ABR47449 Breast ca
73	10	2.5	425	6	ABP81919	ABP81919 Human thr
74	10	2.5	425	7	ADE58075	ADE58075 Human pro
75	10	2.5	425	7	ADG89876	ADG89876 Human pro
76	10	2.5	425	7	ADL14208	ADL14208 Novel hum
77	10	2.5	425	8	ADN04016	ADN04016 Antipsoi
78	10	2.5	425	8	AD029309	AD029309 Human GPC
79	10	2.5	425	8	AD018985	AD018985 Human sof
80	10	2.5	425	8	ADR45608	ADR45608 Human G-P
81	10	2.5	425	8	ADSR4489	ADSR4489 Human pro
82	10	2.5	426	3	AAV45035	AAV45035 Human thr
83	10	2.5	430	8	AD029310	AD029310 Mouse GPC
84	10	2.5	432	7	ADE58073	ADE58073 Rat Prote
85	10	2.5	432	7	ADE58069	ADE58069 Rat Prote
86	10	2.5	892	2	AAW16314	AAW16314 Human thr
87	10	2.5				

## ALIGNMENTS

RESULT 1  
ID AAR66923 standard; protein; 397 AA.  
XX AAR66923;  
AC  
XX